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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2009; month=12; day=22; hr=7; min=36; sec=29; ms=626;]

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Application No: 10575640 Version No: 2.0

Input Set:

Output Set:

Started: 2009-12-02 14:52:57.887
Finished: 2009-12-02 14:52:59.820
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 933 ms
Total Warnings: 6
Total Errors: 0
No. of SeqIDs Defined: 66
Actual SeqID Count: 66

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
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SEQUENCE LISTING

<110> TURECI, Ozlem
SAHIN, Ugar
KREITER, Sebastian

<120> Recombinant Vaccines and Use Thereof

<130> VOS-120

<140> 10575640
<141> 2009-12-02

<150> PCT/EP2004/011512

<151> 2004-10-13

<150> DE 103 47 710.1

<151> 2003-10-14

<160> 66

<170> PatentIn version 3.1

<210> 1

<211> 78

<212> DNA

<213> Homo sapiens

<400> 1

atgcgggtca cggcgcccg aaccctcatac ctgctgctct cgggagccct ggccctgacc 60

gagacctggg ccggctcc 78

<210> 2

<211> 26

<212> PRT

<213> Homo sapiens

<400> 2

Met Arg Val Thr Ala Pro Arg Thr Leu Ile Leu Leu Leu Ser Gly Ala

1 5 10 15

Leu Ala Leu Thr Glu Thr Trp Ala Gly Ser

20 25

<210> 3

<211> 168

<212> DNA

<213> Homo sapiens

<400> 3

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gctactgtga tgtgttaggag gaagagctca ggtggaaaag gagggagcta ctctcaggct 120

gcgtccagcg acagtgccca gggctctgat gtgtctctca cagcttga 168

<210> 4

<211> 55

<212> PRT

<213> Homo sapiens

<400> 4

Ile Val Gly Ile Val Ala Gly Leu Ala Val Leu Ala Val Val Val Ile
1 5 10 15

Gly Ala Val Val Ala Thr Val Met Cys Arg Arg Lys Ser Ser Gly Gly
20 25 30

Lys Gly Gly Ser Tyr Ser Gln Ala Ala Ser Ser Asp Ser Ala Gln Gly
35 40 45

Ser Asp Val Ser Leu Thr Ala
50 55

<210> 5

<211> 129

<212> DNA

<213> Homo sapiens

<400> 5

cagagcaaga tgctgagtgg agtcgggggc tttgtgtgg gcctgcttt cttggggcc 60

ggctgttca tctacttcag gaatcagaaa ggacactctg gacttcagcc aagaggattc 120

ctgagctga 129

<210> 6

<211> 42

<212> PRT

<213> Homo sapiens

<400> 6

Gln Ser Lys Met Leu Ser Gly Val Gly Gly Phe Val Leu Gly Leu Leu
1 5 10 15

Phe Leu Gly Ala Gly Leu Phe Ile Tyr Phe Arg Asn Gln Lys Gly His
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Ser Gly Leu Gln Pro Arg Gly Phe Leu Ser

35

40

<210> 7

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA of restriction site in human HLA class I domains

<400> 7

ctgcagggtcg actctagagg atcc 24

<210> 8

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Restriction site in human HLA class I domains

<400> 8

Leu Gln Val Asp Ser Arg Gly Ser

1

5

<210> 9

<211> 1683

<212> DNA

<213> Human cytomegalovirus

<400> 9

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ctcctgcaga cgggtatcca cgtacgcgtg agccagccct cgctgatctt ggtatgcag 180

tacacgcccc actcgacgccc atgccaccgc ggcgacaatc agctgcaggt gcagcacacg 240

tactttacgg gcagcgaggt ggagaacgtg tcggtaaacg tgcacaaccc cacggggcga 300

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ggt	1683

<210> 10
 <211> 561
 <212> PRT
 <213> Human cytomegalovirus

<400> 10

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20	25	30

Pro Val Leu Pro His Glu Thr Arg Leu Leu Gln Thr Gly Ile His Val		
35	40	45

Arg Val Ser Gln Pro Ser Leu Ile Leu Val Ser Gln Tyr Thr Pro Asp
50 55 60

Ser Thr Pro Cys His Arg Gly Asp Asn Gln Leu Gln Val Gln His Thr
65 70 75 80

Tyr Phe Thr Gly Ser Glu Val Glu Asn Val Ser Val Asn Val His Asn
85 90 95

Pro Thr Gly Arg Ser Ile Cys Pro Ser Gln Glu Pro Met Ser Ile Tyr
100 105 110

Val Tyr Ala Leu Pro Leu Lys Met Leu Asn Ile Pro Ser Ile Asn Val
115 120 125

His His Tyr Pro Ser Ala Ala Glu Arg Lys His Arg His Leu Pro Val
130 135 140

Ala Asp Ala Val Ile His Ala Ser Gly Lys Gln Met Trp Gln Ala Arg
145 150 155 160

Leu Thr Val Ser Gly Leu Ala Trp Thr Arg Gln Gln Asn Gln Trp Lys
165 170 175

Glu Pro Asp Val Tyr Tyr Ser Ala Phe Val Phe Pro Thr Lys Asp
180 185 190

Val Ala Leu Arg His Val Val Cys Ala His Glu Leu Val Cys Ser Met
195 200 205

Glu Asn Thr Arg Ala Thr Lys Met Gln Val Ile Gly Asp Gln Tyr Val
210 215 220

Lys Val Tyr Leu Glu Ser Phe Cys Glu Asp Val Pro Ser Gly Lys Leu
225 230 235 240

Phe Met His Val Thr Leu Gly Ser Asp Val Glu Glu Asp Leu Thr Met
245 250 255

Thr Arg Asn Pro Gln Pro Phe Met Arg Pro His Glu Arg Asn Gly Phe
260 265 270

Thr Val Leu Cys Pro Lys Asn Met Ile Ile Lys Pro Gly Lys Ile Ser

275

280

285

His Ile Met Leu Asp Val Ala Phe Thr Ser His Glu His Phe Gly Leu
290 295 300

Leu Cys Pro Lys Ser Ile Pro Gly Leu Ser Ile Ser Gly Asn Leu Leu
305 310 315 320

Met Asn Gly Gln Gln Ile Phe Leu Glu Val Gln Ala Ile Arg Glu Thr
325 330 335

Val Glu Leu Arg Gln Tyr Asp Pro Val Ala Ala Leu Phe Phe Asp
340 345 350

Ile Asp Leu Leu Leu Gln Arg Gly Pro Gln Tyr Ser Glu His Pro Thr
355 360 365

Phe Thr Ser Gln Tyr Arg Ile Gln Gly Lys Leu Glu Tyr Arg His Thr
370 375 380

Trp Asp Arg His Asp Glu Gly Ala Ala Gln Gly Asp Asp Asp Val Trp
385 390 395 400

Thr Ser Gly Ser Asp Ser Asp Glu Glu Leu Val Thr Thr Glu Arg Lys
405 410 415

Thr Pro Arg Val Thr Gly Gly Ala Met Ala Gly Ala Ser Thr Ser
420 425 430

Ala Gly Arg Lys Arg Lys Ser Ala Ser Ser Ala Thr Ala Cys Thr Ser
435 440 445

Gly Val Met Thr Arg Gly Arg Leu Lys Ala Glu Ser Thr Val Ala Pro
450 455 460

Glu Glu Asp Thr Asp Glu Asp Ser Asp Asn Glu Ile His Asn Pro Ala
465 470 475 480

Val Phe Thr Trp Pro Pro Trp Gln Ala Gly Ile Leu Ala Arg Asn Leu
485 490 495

Val Pro Met Val Ala Thr Val Gln Gly Gln Asn Leu Lys Tyr Gln Glu
500 505 510

Phe Phe Trp Asp Ala Asn Asp Ile Tyr Arg Ile Phe Ala Glu Leu Glu
515 520 525

Gly Val Trp Gln Pro Ala Ala Gln Pro Lys Arg Arg Arg His Arg Gln
530 535 540

Asp Ala Leu Pro Gly Pro Cys Ile Ala Ser Thr Pro Lys Lys His Arg
545 550 555 560

Gly

<210> 11
<211> 1962
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA encoding human HLA class I domains and CMV pp65

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cgccgttgtc ccgaaatgat atccgtactg ggtcccatatt cggggcacgt gctgaaagcc 180
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caggagccca tgtcgatcta tgtgtacgctg ctgcccgtca agatgtgaa catccccagc 480
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aagatctcg acatcatgct ggatgtggct ttacacctac acgagcattt tgggctgctg	1020
tgtcccaaga gcatcccgaa cctgagcatc tcaggttaacc tggatgaa cgggcagcag	1080
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gaccggcacg acgaggggtgc cgcccaggc gacgacgacg tctggaccag cggatcgac	1320
tccgacgaag aactcgtaac caccgagcgc aagacgcccc gcgtcaccgg cggcggcgcc	1380
atggcggggcg cctccacttc cgccggccgc aaacgcaaat cagcatcctc ggcgacggcg	1440
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gaggacaccc acgaggattc cgacaacgaa atccacaatc cggccgtgtt cacctggccg	1560
ccctggcagg ccggcatcct ggcccgcaac ctggtgccca tgggtggctac ggttcagggt	1620
cagaatctga agtaccagga attcttctgg gacgccaacg acatctaccg catcttcgccc	1680
gaatttggaaag gcgtatggca gcccgtcgca aacccaaac gtcgcccaca ccggcaagac	1740
gccttggcccg ggccatgcat cgccctcgacg cccaaaaagc accgaggtgg atccatcgta	1800
ggcattgttg ctggctggc tgccttagca gttgtggta tcggagctgt ggtcgctact	1860
gtgatgtgta ggaggaagag ctcaggtgga aaaggaggga gctactctca ggctgcgtcc	1920
agcgacagtg cccaggggctc tgatgtgtct ctcacagctt ga	1962

<210> 12
 <211> 653
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Fusion protein of human HLA class I domains and CMV pp65
 <400> 12

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Leu Ala Leu Thr Glu Thr Trp Ala Gly Ser Leu Gln Val Asp Ser Arg		
20	25	30

Gly Ser Thr Met Glu Ser Arg Gly Arg Arg Cys Pro Glu Met Ile Ser		
35	40	45

Val Leu Gly Pro Ile Ser Gly His Val Leu Lys Ala Val Phe Ser Arg
50 55 60

Gly Asp Thr Pro Val Leu Pro His Glu Thr Arg Leu Leu Gln Thr Gly
65 70 75 80

Ile His Val Arg Val Ser Gln Pro Ser Leu Ile Leu Val Ser Gln Tyr
85 90 95

Thr Pro Asp Ser Thr Pro Cys His Arg Gly Asp Asn Gln Leu Gln Val
100 105 110

Gln His Thr Tyr Phe Thr Gly Ser Glu Val Glu Asn Val Ser Val Asn
115 120 125

Val His Asn Pro Thr Gly Arg Ser Ile Cys Pro Ser Gln Glu Pro Met
130 135 140

Ser Ile Tyr Val Tyr Ala Leu Pro Leu Lys Met Leu Asn Ile Pro Ser
145 150 155 160

Ile Asn Val His His Tyr Pro Ser Ala Ala Glu Arg Lys His Arg His
165 170 175

Leu Pro Val Ala Asp Ala Val Ile His Ala Ser Gly Lys Gln Met Trp
180 185 190

Gln Ala Arg Leu Thr Val Ser Gly Leu Ala Trp Thr Arg Gln Gln Asn
195 200 205

Gln Trp Lys Glu Pro Asp Val Tyr Tyr Thr Ser Ala Phe Val Phe Pro
210 215 220

Thr Lys Asp Val Ala Leu Arg His Val Val Cys Ala His Glu Leu Val
225 230 235 240

Cys Ser Met Glu Asn Thr Arg Ala Thr Lys Met Gln Val Ile Gly Asp
245 250 255

Gln Tyr Val Lys Val Tyr Leu Glu Ser Phe Cys Glu Asp Val Pro Ser
260 265 270

Gly Lys Leu Phe Met His Val Thr Leu Gly Ser Asp Val Glu Glu Asp
275 280 285

Leu Thr Met Thr Arg Asn Pro Gln Pro Phe Met Arg Pro His Glu Arg
290 295 300

Asn Gly Phe Thr Val Leu Cys Pro Lys Asn Met Ile Ile Lys Pro Gly
305 310 315 320

Lys Ile Ser His Ile Met Leu Asp Val Ala Phe Thr Ser His Glu His
325 330 335

Phe Gly Leu Leu Cys Pro Lys Ser Ile Pro Gly Leu Ser Ile Ser Gly
340 345 350

Asn Leu Leu Met Asn Gly Gln Gln Ile Phe Leu Glu Val Gln Ala Ile
355 360 365

Arg Glu Thr Val Glu Leu Arg Gln Tyr Asp Pro Val Ala Ala Leu Phe
370 375 380

Phe Phe Asp Ile Asp Leu Leu Gln Arg Gly Pro Gln Tyr Ser Glu
385 390 395 400

His Pro Thr Phe Thr Ser Gln Tyr Arg Ile Gln Gly Lys Leu Glu Tyr
405 410 415

Arg His Thr Trp Asp Arg His Asp Glu Gly Ala Ala Gln Gly Asp Asp
420 425 430

Asp Val Trp Thr Ser Gly Ser Asp Ser Asp Glu Glu Leu Val Thr Thr
435 440 445

Glu Arg Lys Thr Pro Arg Val Thr Gly Gly Ala Met Ala Gly Ala
450 455 460

Ser Thr Ser Ala Gly Arg Lys Arg Lys Ser Ala Ser Ser Ala Thr Ala
465 470 475 480

Cys Thr Ser Gly Val Met Thr Arg Gly Arg Leu Lys Ala Glu Ser Thr
485 490 495

Val Ala Pro Glu Glu Asp Thr Asp Glu Asp Ser Asp Asn Glu Ile His
500 505 510

Asn Pro Ala Val Phe Thr Trp Pro Pro Trp Gln Ala Gly Ile Leu Ala
515 520 525

Arg Asn Leu Val Pro Met Val Ala Thr Val Gln Gly Gln Asn Leu Lys
530 535 540

Tyr Gln Glu Phe Phe Trp Asp Ala Asn Asp Ile Tyr Arg Ile Phe Ala
545 550 555 560

Glu Leu Glu Gly Val Trp Gln Pro Ala Ala Gln Pro Lys Arg Arg Arg
565 570 575

His Arg Gln Asp Ala Leu Pro Gly Pro Cys Ile Ala Ser Thr Pro L